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	10	20	30	40	50	
NOV_HU	MQSVQSTSFCLRKQCLCLTFLLLHLLGQVAAT-----					32
CTGF_H	MTAASMGPRVAVFVLLALCSRPAVG-----					26
zctgf2M	-----					0
zctgf4H	MQGLLFPTLLLAGLAQFCCRVQG-----TGPLDTTPEGRP					35
IBP1_H	MSEVPVARVWLVLVLLLTQVQGVTAG-----					25
IBP2_H	MLPRVGCPALPLPPPPLPLPLLLLLLLGASG-GGGGARAEVLFRCPPCT					49
	60	70	80	90	100	
NOV_HU	-----QRCPPQCPGRCPATP-PTCAPGVRAVLGDCSCCLVCARQR					71
CTGF_H	-----QNCSGPCR--CPDEPAPRCPAGVSLVLDGCGCCRVCAKQL					64
zctgf2M	-----					0
zctgf4H	GEVSDAPQRKQFCHWPCK--CPQQK-PRCPPGVSLVRDGCCKICAKQP					82
IBP1_H	---APWQCAPCSAEKLAL--CPPVS-ASCSEVTR--SAGCGCCPMCALPL					67
IBP2_H	PERLAACGPPPVAPPAAVAAGGARMPCAEVLR--EPGCGCCSVCARLE					97
	110	120	130	140	150	
NOV_HU	GESCSLEPCDESSGLYCDRSADPSN-QTGICTAVEGD-NCVFDGVIYRS					119
CTGF_H	GELCTERDPCDPHKGLFCDFGSPANR-KIGVCTAKDGA-PCIFGGTVYRS					112
zctgf2M	-----					0
zctgf4H	GEICNEADLCDPHKGLYCDYSVDRPRYETGVCAYLAV-GCEFNQVHYHN					131
IBP1_H	GAACGVATARCARGLSR-----					85
IBP2_H	GEACGVYTPRCGQGLRCY-----					115
	160	170	180	190	200	
NOV_HU	GEKFQPSCKFQCTCRDQGIGCVPRQLDVLLPEPNCAPARKVEVPGECCCE					169
CTGF_H	GESFQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPFPRRVKLPKGCCE					162
zctgf2M	-----					0
zctgf4H	GQVFQPNPLFSCLCVSGAIGCTPL--FIPKLAGSHCSGAK---GGKKSD					175
IBP1_H	-----					85
IBP2_H	-----					115
	210	220	230	240	250	
NOV_HU	KWICGPDEEDSLGGL---TLAAYRPEATLGVEVSDSSVNCIEQTTEWTAC					216
CTGF_H	EWVC--DEPK-DQTVVGPALAAAYRLEDTFGPDPTMIRANCLVQTTEWSAC					209
zctgf2M	-----NVVYLPAYRNLPLIWKKKCLVQATKWTPC					29
zctgf4H	QSNC--SLEP---LLQQLSTS YKTM PAYRNLPLIWKKKCLVQATKWTPC					219
IBP1_H	-----					85
IBP2_H	-----					115

Fig. 1A

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	260	270	280	290	300	
NOV_HU	SKSCGMGFSTRVTNRNRQCEMLKQTRL	CMVRPCEQEPEQ-PTDKKGKKCL				265
CTGF_H	SKTCGMGISTRVTNDNASCRLEKQSRL	CMVRPCEADLE--ENIKKGKKCI				257
ZCTGF2M	S-----				IPRGETCQ	38
zctgf4H	SRTC GMGISNRVTNENSNC	EMRKEKRLCYIQPCDSN	ILKTIKIPKGKTCQ			269
IBP1_H	-----					85
IBP2_H	-----					115
	310	320	330	340	350	
NOV_HU	RT-KKSLKAIHLQFKNCTSLHTYKPRFC	GVCS DGRCTPHNTKTIQAEFQ				314
CTGF_H	RTPKISKPIKFE-LSGCTSMKTYRAKFC	GVCTDGRCTPHRTTTL PVEFK				306
ZCTGF2M	PTFQLPKAEKFV-FSGCSSTQSYRPTFC	GICLDKRCCVPNKS KMITVRFD				87
zctgf4H	PTFQLSKAEKFV-FSGCSSTQSYKPTFC	GICLDKRCCIPNKS KMITIQFD				318
IBP1_H	-----					85
IBP2_H	-----					115
	360	370	380	390		
NOV_HU	CSPGQIVKKPVMVIGTCTCHTNCPKNNEA	FLQELELKTTRGK--				356
CTGF_H	CPDGEVMKKNNMMFIKTCACHYNCPGDND	IFESLYRKMYGDM--				348
ZCTGF2M	CPSEGSFKWQMLWVTSCVCQRDCREPGDI	FSEL RIL-----				123
zctgf4H	CPNEGSFKWKMLWITSCVCQRNCREPGDI	FSELKIL-----				354
IBP1_H	-----					85
IBP2_H	-----					115

Fig. 1B